

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2003, 13:01:34 ; Search time 2 Seconds

(without alignments)  
2.904 Million cell updates/sec

Title: us-10-036-041-1

Perfect score: 1712  
Sequence: 1 ggcacgtgccgagagacc.....ttgttaagataaaaaaaa 1712

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1696 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Database : us-09-552-225a-1.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1696	99.1	1696	1	us-09-552-225a-1

#### ALIGNMENTS

RESULT 1					
us-09-552-225a-1					
Query Match 99.1%; Score 1696; DB 1; Length 1696;					
Best Local Similarity 100.0%; Pred. No. 0;					
Matches 1696; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	9	CCCGAGGAGACACCGCTCTGGAGCTCTGCTCTCTCAGGAGACTCTGAGGCTCTGT	68		
DB	1	CCCGAGGAGACACCGCTCTGGAGCTCTGCTCTCTCAGGAGACTCTGAGGCTCTGT	60		
QY	69	TCAGAAATCATGCTTTGGAGGAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTCTCTC	128		
DB	61	TCAGAAATCATGCTTTGGAGGAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTCTCTC	120		
QY	129	CTTTTTCCTCTGCTCAAGATGAATACATGGAGTCTCCAAACCCGGAGGACTACCCCCAG	188		
DB	121	CTTTTTCCTCTGCTCAAGATGAATACATGGAGTCTCCAAACCCGGAGGACTACCCCCAG	180		
QY	189	ACTGCACTAGTCTTCTGAGAGACTACAGCTTTTCAGGCTACCAAGGCCCTCCCTGGGC	248		
DB	181	ACTGCACTAGTCTTCTGAGAGACTACAGCTTTTCAGGCTACCAAGGCCCTCCCTGGGC	240		
QY	249	CACCGGGCCCTCTGCGCATTCCAGGAACCATGGAACAAATGGCAATGGAGGCCACTG	308		
DB	241	CACCGGGCCCTCTGCGCATTCCAGGAACCATGGAACAAATGGCAATGGAGGCCACTG	300		

QY	309	GTCTATGAAGAGGCCAAAGGTGAGAGGGCGCAAAAGGTGACCTGGGGCCTCGAGGGGAGC	368		
DB	301	GTCTATGAAGAGGCCAAAGGTGAGAGGGCGCAAAAGGTGACCTGGGGCCTCGAGGGGAGC	360		
QY	369	GGGGGAGGAGTGGCCCAAGGAGAGAGGGCTTACCCGGGGATCCACCAAGACTTCAGA	428		
DB	361	GGGGGAGGAGTGGCCCAAGGAGAGAGGGCTTACCCGGGGATCCACCAAGACTTCAGA	420		
QY	429	TTGCATTATGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTCATCTCA	488		
DB	421	TTGCATTATGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTCATCTCA	480		
QY	489	GCAGTGTGAGACCAACATTTGAACTTCTTGTATGTCAATGAGTGGTGGGCCCC	548		
DB	481	GCAGTGTGAGACCAACATTTGAACTTCTTGTATGTCAATGAGTGGTGGGCCCC	540		
QY	549	CAGTATCAGGTGTATTTCTTCACCTTCAGCATGATGAGCATGAGGATGTTGAGGAAG	608		
DB	541	CAGTATCAGGTGTATTTCTTCACCTTCAGCATGATGAGCATGAGGATGTTGAGGAAG	600		
QY	609	TGTATGTACCTTATGCAATGCGCAACACAGCTTTCAGCATGTACAGCTATGAAATGA	668		
DB	601	TGTATGTACCTTATGCAATGCGCAACACAGCTTTCAGCATGTACAGCTATGAAATGA	660		
QY	669	AGGGCAAAATCAGATACATCAGCAATCATGCTGTGTGAAGCTAGCCAAAGGGATGAGG	728		
DB	661	AGGGCAAAATCAGATACATCAGCAATCATGCTGTGTGAAGCTAGCCAAAGGGATGAGG	720		
QY	729	TTTGGCTGGAATGGGCAATGGGCTCTCCATGSGGACCAACACGCTTCTCCACCTTTG	788		
DB	721	TTTGGCTGGAATGGGCAATGGGCTCTCCATGSGGACCAACACGCTTCTCCACCTTTG	780		
QY	789	CAGGATTCCTGCTCTTTGAACTTAAGTAAATATATGACTAGATAGCTCCACTTTGGGA	848		
DB	781	CAGGATTCCTGCTCTTTGAACTTAAGTAAATATATGACTAGATAGCTCCACTTTGGGA	840		
QY	849	AGACTTTGAGCTGAGCTGATTTGTAGATCTGAGGAACATTTAAAGTTGAGGGTTTACA	908		
DB	841	AGACTTTGAGCTGAGCTGATTTGTAGATCTGAGGAACATTTAAAGTTGAGGGTTTACA	900		
QY	909	TTGCTGTATTCAAAAATTTATTTGTTGCAATGTTGTTGCGCTACAGGTACACCAATAAT	968		
DB	901	TTGCTGTATTCAAAAATTTATTTGTTGCAATGTTGTTGCGCTACAGGTACACCAATAAT	960		
QY	969	GTGGACAATTCAGGGGCTCAGAAAGATCAACCAACAAATAGTCTTCTCAGATGACCTTG	1028		
DB	961	GTGGACAATTCAGGGGCTCAGAAAGATCAACCAACAAATAGTCTTCTCAGATGACCTTG	1020		
QY	1029	ACTAATATCTCAGCAATCTTTATCAGCTCTTCTTGGCAGCTAAAAGATTAATTCCTCT	1088		
DB	1021	ACTAATATCTCAGCAATCTTTATCAGCTCTTCTTGGCAGCTAAAAGATTAATTCCTCT	1080		
QY	1089	GAGCAGGTGGAAATATTTTCTATCAGCAAGTCAATTCGAAGAATTTTGTACTAC	1148		
DB	1081	GAGCAGGTGGAAATATTTTCTATCAGCAAGTCAATTCGAAGAATTTTGTACTAC	1140		
QY	1149	TCGCTTTTAAATTAATACAGTTTTCAGSAACCCCTGAGTTTAAAGTTTCAATTTCTT	1208		
DB	1141	TCGCTTTTAAATTAATACAGTTTTCAGSAACCCCTGAGTTTAAAGTTTCAATTTCTT	1200		
QY	1209	TATAACATTTGAGAGAAATCGGATGTAGTATGATGACAGGCTGGGCAAGACAGGGGCA	1268		
DB	1201	TATAACATTTGAGAGAAATCGGATGTAGTATGATGACAGGCTGGGCAAGACAGGGGCA	1260		
QY	1269	CTAGCTGCTTATTTAGCTAATTTAGTGCCTCGCTGTTGAGCTTAGCTTTGACCTTTTC	1328		
DB	1261	CTAGCTGCTTATTTAGCTAATTTAGTGCCTCGCTGTTGAGCTTAGCTTTGACCTTTTC	1320		
QY	1329	CTTTTGATCCAAAAATACATTTAAACTCTGAATTCACATACATGCTATTTTAAAGTCA	1388		
DB	1321	CTTTTGATCCAAAAATACATTTAAACTCTGAATTCACATACATGCTATTTTAAAGTCA	1380		
QY	1389	ATAGATTTTAGCTATTAAGTGTGCTTACAGTAAATGTTGTTGTAATTTTGTATGTTCC	1448		



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Search completed: August 6, 2003, 13:03:18  
Job time : 0.001 secs

OM protein - protein search, using sw model

Run on: August 6, 2003, 13:03:18 ; Search time 0.001 Seconds  
(without alignments)  
60.516 Million cell updates/sec

Title: us-10-036-041-2  
Perfect score: 1367  
Sequence: 1 MLWRQLIYWQLLALFFLPFC.....LHGDHQRSTFAGFLLPETK 246

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 246 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1 summaries

Database : us-09-552-225a-2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1367	100.0	246	1	us-09-552-225a-2

ALIGNMENTS

RESULT 1  
us-09-552-225a-2

Query Match	100.0%	Score 1367;	DB 1;	Length 246;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 246;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLWRQLIYWQLLALFFLPFC	CODEYMES	POTGGLPPDCSKCHGDSFRGYGGPPGPG 60
DB	1	MLWRQLIYWQLLALFFLPFC	CODEYMES	POTGGLPPDCSKCHGDSFRGYGGPPGPG 60
QY	61	PGIPGNHGNNGNNGATGHEGAKGKGD	GLGPRGERGOGHGPKEGYPGIPPELQIAF	120
DB	61	PGIPGNHGNNGNNGATGHEGAKGKGD	GLGPRGERGOGHGPKEGYPGIPPELQIAF	120
QY	121	MASLATHFNSQNSGIIFSSVETNIGNFF	VDYMTGRFGAPVSGYVFFTFSMKKHEDVEEVY	180
DB	121	MASLATHFNSQNSGIIFSSVETNIGNFF	VDYMTGRFGAPVSGYVFFTFSMKKHEDVEEVY	180
QY	181	YLMHNGTWFVSMYSYEMKGS	DTSSNHAUHLAKGDEVWLRMGNGALHGDHQRSTFAGF	240
DB	181	YLMHNGTWFVSMYSYEMKGS	DTSSNHAUHLAKGDEVWLRMGNGALHGDHQRSTFAGF	240
QY	241	LLFETK	246	
DB	241	LLFETK	246	